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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=22; hr=12; min=45; sec=12; ms=146;]

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Reviewer Comments:

Leu Glu Phe
30

Tyr Thr Lys Arg Leu Phe Gln Ser Val Ser Pro Ser Phe Leu Ser Ile
35 40 45

Please correct invalid amino acid numbering shown above in sequence id# 48. Please check the remaining sequences for similar errors.

Application No: 10785116 Version No: 3.0

Input Set:

Output Set:

Started: 2009-01-07 15:10:48.392
Finished: 2009-01-07 15:10:52.884
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 492 ms
Total Warnings: 33
Total Errors: 9
No. of SeqIDs Defined: 49
Actual SeqID Count: 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 201	Mandatory field data missing in <223> in SEQ ID (11)
E 201	Mandatory field data missing in <223> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

Input Set:

Output Set:

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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occurred more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (45)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (35)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (36)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (40)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (41)
E 323	Invalid/missing amino acid numbering SEQID (48) at Protein (45)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (46)

SEQUENCE LISTING

<110> Pecker, Iris
Vlodavsky , Israel
Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

<130> 27674

<140> 10785116
<141> 2004-02-25

<160> 49

<170> PatentIn version 3.1

<210> 1
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 1
ccatcctaat acgactcaact atagggc

27

<210> 2
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<220>
<223> Synthetic oligonucleotide

<400> 2
gtagtgtatgc catgttaactg aatc

24

<210> 3
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<220>
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<400> 3
actcaactata gggctcgagc ggc

23

<210> 4
<211> 22
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<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 4
gcatcttagc cgtcttctt cg 22

<210> 5

<211> 15

<212> DNA

<213> Artificial sequence

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<223> Synthetic oligonucleotide

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<211> 23

<212> DNA

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<223> Synthetic oligonucleotide

<400> 6
ttcgatccca agaaggaaatc aac 23

<210> 7

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 7
gtagtgtatgc catgtactg aatc 24

<210> 8

<211> 9

<212> PRT

<213> Artificial sequence

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<223> Peptide derived from tryptic digestion of human heparanase

<400> 8

Tyr Gly Pro Asp Val Gly Gln Pro Arg

<210> 9
<211> 1721
<212> DNA
<213> Homo sapiens

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<211> 543
<212> PRT
<213> Homo sapiens

<400> 10

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Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Val Leu Tyr Thr Phe
165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
195 200 205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
225 230 235 240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
355 360 365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
370 375 380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
500 505 510

Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
515 520 525

Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
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<210> 11
<211> 1721
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (63)..(1691)
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Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu

1	5	10	15	
ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga				155
Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg				
20	25	30		
cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag				203
Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu				
35	40	45		
ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc				251
Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala				
50	55	60		
aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag				299
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys				
65	70	75		
ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt				347
Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly				
80	85	90	95	
ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc				395
Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr				
100	105	110		
ttt gaa gag aga agt tac tggcaa tct caa gtc aac cag gat att tgc				443
Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys				
115	120	125		
aaa tat gga tcc atc cct gat gtg gag gag aag tta cgg ttg gaa				491
Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu				
130	135	140		
tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag				539
Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys				
145	150	155		
ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act				587
Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr				
160	165	170	175	
ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta				635
Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu				
180	185	190		
tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc				683
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu				
195	200	205		
ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc				731
Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly				
210	215	220		
aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg				779
Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly				
225	230	235		

tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag			827
Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys			
240	245	250	255
tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct			875
Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro			
260	265	270	
cga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga			923
Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly			
275	280	285	
gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg			971
Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg			
290	295	300	
act gct acc agg gaa gat ttt cta aac cct gat gta ttg gac att ttt			1019
Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe			
305	310	315	
att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct			1067
Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro			
320	325	330	335
ggc aag aag gtc tgg tta gga gaa aca agc tct gca tat gga ggc gga			1115
Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly			
340	345	350	
gcg ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat			1163
Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp			
355	360	365	
aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa			1211
Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln			
370	375	380	
gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat			1259
Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp			
385	390	395	
cct tta cct gat tat tgg cta tct ctt ctg ttc aag aaa ttg gtg ggc			1307
Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly			
400	405	410	415
acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt			1355
Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu			
420	425	430	
cga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa gaa			1403
Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu			
435	440	445	
gga gat tta act ctg tat gcc ata aac ctc cat aac gtc acc aag tac			1451
Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr			
450	455	460	

